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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 09:48:28 ; Search time 1166.08 Seconds
(without alignments)
11181.073 Million cell updates/sec

Title: US-09-922-895-4

Perfect score: 448
Sequence: 1 TAGTCAGATGCGAATAATT.....CCCTGCTTAATGAAAGCTT 448

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
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16: em_fun:*
17: em_hum:*
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22: em_ov:*
23: em_pat:*
24: em_ph:*
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26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	448	100.0	448	6	ARI64121	ARI64121 Sequence
2	448	100.0	448	6	AX030931	AX030931 Sequence
3	448	100.0	1717	6	AX334894	AX334894 Sequence
4	448	100.0	1717	6	HS051241	U51241 Human eosin
5	448	100.0	1915	6	BD006761	BD006761 Chemokine
6	448	100.0	5791	9	AF247361	AF247361 Homo sapi
7	448	100.0	197279	9	AC104439	AC104439 Homo sapi
8	448	100.0	220965	2	HS012688	AJ312688 Homo sapi
9	380.4	84.9	1689	9	HS049727	U49727 Human C-C C
10	339.2	75.7	7201	6	AX345239	AX345239 Sequence
11	294.4	65.7	7201	6	AX345238	AX345238 Sequence
12	111.2	24.8	320202	2	AC095857	AC095857 Rattus no
13	105	23.4	1201	9	HS028694	U28694 Human eosin
14	56.2	12.5	1440	10	MM028406	U28406 Mus muscu
15	48.4	10.8	349980	6	AX344574	AX344574 Sequence
16	47.4	10.6	168406	2	AC090770	AC090770 Homo sapi
17	47.4	10.6	168476	9	AC011260	AC011260 Homo sapi
18	47.4	10.6	170337	2	AP001378	AP001378 Homo sapi
19	46.8	10.4	7025	6	AX339179	AX339179 Sequence
20	46.8	10.4	7025	6	AX348447	AX348447 Sequence
21	45.8	10.2	470	3	AF379870	AF379870 Baryconus
22	45.4	10.1	349980	6	AX344551	AX344551 Sequence
23	45.2	10.1	125395	9	AC072022	AC072022 Homo sapi
24	45.2	10.1	196408	2	AC130420	AC130420 Homo sapi
25	45.2	10.1	196758	2	AC009653	AC009653 Homo sapi
26	44.4	9.9	44724	2	AC115385	AC115385 Dictyoste
27	44.2	9.9	100000	9	AP000205	AP000205 Homo sapi
28	44.2	9.9	110715	9	HS197316	AP000127 Homo sapi
29	44.2	9.9	149898	9	AP000244	AP000244 Homo sapi
30	44.2	9.9	165865	2	AC079958	AC079958 Mus muscu
31	44.2	9.9	188661	2	AC093705	AC093705 Papio cyn
32	44.2	9.9	193552	2	AC021569	AC021569 Homo sapi
33	44.2	9.9	197843	2	AC024373	AC024373 Homo sapi
34	44.2	9.9	340000	9	AP001709	AP001709 Homo sapi
35	43.8	9.8	281892	2	AC125486	AC125486 Mus muscu
36	43.6	9.7	8720	9	AC096578	AC096578 Homo sapi
37	43.6	9.7	156069	9	AC079256	AC079256 Homo sapi
38	43.6	9.7	349980	6	AX344558	AX344558 Sequence
39	43.4	9.7	107739	2	AC116979	AC116979 Dictyoste
40	43.4	9.7	121210	9	AL607022	AL607022 Human DNA
41	43.4	9.7	126579	9	AC004692	AC004692 Homo sapi
42	43.2	9.6	61028	2	AC087270	AC087270 Homo sapi
43	43.2	9.6	63849	9	AC093378	AC093378 Homo sapi
44	43.2	9.6	121019	9	AL354715	AL354715 Human DNA
45	43.2	9.6	121019	9	AL354715	AL354715 Human DNA

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
ARI64121	ARI64121	Sequence 4 from patent US 6271347.	ARI64121	ARI64121.1	GI:16235067	Unknown.	Unclassified.	1 (bases 1 to 448)	Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.	Eosinophil ecotaxin receptor	Patent: US 6271347-A 4 07-AUG-2001;	Location/Qualifiers

source	1. 448	/organism="unknown"
BASE COUNT	155 a 98 c 70 g	125 t
ORIGIN		
Query Match	100.0%;	Score 448; DB 6; Length 448;
Best Local Similarity	100.0%;	Pred. No. 3.7e-88;
Matches 448;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 TAGGTGATGTCAGAAAATTTGCTTAAAGAGAGAACCAAGAGATGAGCAACACATT	60
DB	1 TAGGTGATGTCAGAAAATTTGCTTAAAGAGAGAACCAAGAGATGAGCAACACATT	60
QY	61 AAGCCTTCACACTCACTCTTAAACAGTCTTCAACTTCAGTGCACACTGAAGCTC	120
DB	61 AAGCCTTCACACTCACTCTTAAACAGTCTTCAACTTCAGTGCACACTGAAGCTC	120
QY	121 TTGAAGACACTGAAATATPACACAGCAGTACAGTATGATGATGATACCTTAAGTTCATT	180
DB	121 TTGAAGACACTGAAATATPACACAGCAGTACAGTATGATGATGATACCTTAAGTTCATT	180
QY	181 ACCACAGGCCAGGAGGCGTGCGACGCTACTCATCATCAACCCCTTAAAGACAGAGCTTGGCT	240
DB	181 ACCACAGGCCAGGAGGCGTGCGACGCTACTCATCATCAACCCCTTAAAGACAGAGCTTGGCT	240
QY	241 TCTCTCTCTTAAATGAGTTACTACTATTTTAATGCACTGGAATGTTAGTACTTCTATA	300
DB	241 TCTCTCTCTTAAATGAGTTACTACTATTTTAATGCACTGGAATGTTAGTACTTCTATA	300
QY	301 TGCAGCTACAAAAGGTAAACCTTTTATATTTTATATTAATTAAGTTCAGCCAGCTATTGA	360
DB	301 TGCAGCTACAAAAGGTAAACCTTTTATATTTTATATTAATTAAGTTCAGCCAGCTATTGA	360
QY	361 TATTAATAAACAATTTTCACACATPACAAATGAAGTAACTATTATTATTTCTAATGTGCT	420
DB	361 TATTAATAAACAATTTTCACACATPACAAATGAAGTAACTATTATTATTTCTAATGTGCT	420
QY	421 AGTCTCTTCCCTGCTTAATGAAGCTT	448
DB	421 AGTCTCTTCCCTGCTTAATGAAGCTT	448
RESULT 2		
AX030931	448 bp	DNA linear PAT 20-SEP-2000
LOCUS	AX030931	
DEFINITION	Sequence 4 from Patent EP1012190.	
ACCESSION	AX030931	
VERSION	AX030931.1 GI:10278336	
KEYWORDS		
SOURCE	unidentified.	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 448)	
AUTHORS	Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.	
TITLE	Eosinophil ectoxin receptor	
JOURNAL	Patent: EP 1012190-A 4 28-JUN-2000;	
FEATURES	MERCK & CO INC (US)	
source	Location/Qualifiers	
BASE COUNT	155 a 98 c 70 g	125 t
ORIGIN		
Query Match	100.0%;	Score 448; DB 6; Length 448;
Best Local Similarity	100.0%;	Pred. No. 3.7e-88;
Matches 448;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 TAGGTGATGTCAGAAAATTTGCTTAAAGAGAGAACCAAGAGATGAGCAACACATT	60
DB	1 TAGGTGATGTCAGAAAATTTGCTTAAAGAGAGAACCAAGAGATGAGCAACACATT	60
QY	61 AAGCCTTCACACTCACTCTTAAACAGTCTTCAACTTCAGTGCACACTGAAGCTC	120
DB	61 AAGCCTTCACACTCACTCTTAAACAGTCTTCAACTTCAGTGCACACTGAAGCTC	120
QY	121 TTGAAGACACTGAAATATPACACAGCAGTACAGTATGATGATGATACCTTAAGTTCATT	180
DB	121 TTGAAGACACTGAAATATPACACAGCAGTACAGTATGATGATGATACCTTAAGTTCATT	180
QY	181 ACCACAGGCCAGGAGGCGTGCGACGCTACTCATCATCAACCCCTTAAAGACAGAGCTTGGCT	240
DB	181 ACCACAGGCCAGGAGGCGTGCGACGCTACTCATCATCAACCCCTTAAAGACAGAGCTTGGCT	240
QY	241 TCTCTCTCTTAAATGAGTTACTACTATTTTAATGCACTGGAATGTTAGTACTTCTATA	300
DB	241 TCTCTCTCTTAAATGAGTTACTACTATTTTAATGCACTGGAATGTTAGTACTTCTATA	300
QY	301 TGCAGCTACAAAAGGTAAACCTTTTATATTTTATATTAATTAAGTTCAGCCAGCTATTGA	360
DB	301 TGCAGCTACAAAAGGTAAACCTTTTATATTTTATATTAATTAAGTTCAGCCAGCTATTGA	360
QY	361 TATTAATAAACAATTTTCACACATPACAAATGAAGTAACTATTATTATTTCTAATGTGCT	420
DB	361 TATTAATAAACAATTTTCACACATPACAAATGAAGTAACTATTATTATTTCTAATGTGCT	420
QY	421 AGTCTCTTCCCTGCTTAATGAAGCTT	448
DB	421 AGTCTCTTCCCTGCTTAATGAAGCTT	448

Db	61	AAGCCTTCACACTCACCCTCTAAACGATCCCTCAAACTTCCAGTGAACACTGAAGCTC	120
OY	121	TTGAAGACACTGAATATATACACACAGCAGTACAGTACATGATGATACCTTAAGTCAATT	180
Db	121	TTGAAGACACTGAATATATACACACAGCAGTACAGTACATGATGATACCTTAAGTCAATT	180
OY	181	ACCACAGGCGACGGGCTGGGCGAGCGCTACTGCATTCATCAACCCGTAACAGAGGCTTTGCT	240
Db	181	ACCACAGGCGACGGGCTGGGCGAGCGCTACTGCATTCATCAACCCGTAACAGAGGCTTTGCT	240
OY	241	TCTCTCTCTAAATGAGTGTACTACATTTTAAATGACAGCTGAACTGTATGATTACTATA	300
Db	241	TCTCTCTCTAAATGAGTGTACTACATTTTAAATGACAGCTGAACTGTATGATTACTATA	300
OY	301	TGCGGCTACAAAAGAGTAAACCTTTTATATTTATACATTACTTCAGCCAGCTATTGA	360
Db	301	TGCGGCTACAAAAGAGTAAACCTTTTATATTTTATACATTACTTCAGCCAGCTATTGA	360
OY	361	TATATATTAACATTTTCACACAAATACAAATAGTAACTATTTTATTTTCTAATGCTGCT	420
Db	361	TATATATTAACATTTTCACACAAATACAAATAGTAACTATTTTATTTTCTAATGCTGCT	420
OY	421	AGTTCTTTCCCTGCTTAATGAAAAGCTT	448
Db	421	AGTTCTTTCCCTGCTTAATGAAAAGCTT	448
RESULT 3			
LOCUS	AX334894	1717 bp	DNA
DEFINITION	Sequence 5403 from Patent WO0194629.		linear
ACCESSION	AX334894		
KEYWORDS	AX334894.1 GI:18125613		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,		
JOURNAL	Hortigan, S., Soppel, D.R. and Weaver, Z.		
FEATURES	Cancer gene determination and therapeutic screening using signature		
SOURCE	gene sets		
BASE COUNT	Patent: WO 0194629-A 5403 13-DEC-2001;		
ORIGIN	Avalon Pharmaceuticals (US)		
Query Match	Location/Qualifiers		
Best Local Similarity	1. 1717		
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/Organism="Homo sapiens"		
	/db_xref="taxon:9606"		
OY	1	TAGGTCAGATGCGAGAAATTTGGCTTAAGAGGAGGACCAAGAGATGTAAGCAAAACATT	60
Db	1270	TAGGTCAGATGCGAGAAATTTGGCTTAAGAGGAGGACCAAGAGATGTAAGCAAAACATT	1329
OY	61	AAGCCTTCACACTCACCCTCTAAACGATCCTTCAAACCTCCAGTCAAACTGAAGCTC	120
Db	1330	AAGCCTTCACACTCACCCTCTAAACGATCCTTCAAACCTCCAGTCAAACTGAAGCTC	1389
OY	121	TTGAAGACACTGAATATATACACACAGCAGTACAGTACATGATGATACCTTAAGTCAATT	180
Db	1390	TTGAAGACACTGAATATATACACACAGCAGTACAGTACATGATGATGATACCTTAAGTCAATT	1449
OY	181	ACCACAGGCGACGGGCTGGGCGAGCGCTACTGCATTCATCAACCCGTAACAGAGGCTTTGCT	240
Db	1450	ACCACAGGCGACGGGCTGGGCGAGCGCTACTGCATTCATCAACCCGTAACAGAGGCTTTGCT	1509

QY	241	TCTCTCTAAAGAGTACCTACATTTTATGACCGTAGTGGTATGTTACTATA	300
Db	1510	TCTCTCTTAAAGTACCTACATTTTATGACCGTAGTGGTATGTTACTATA	1569
QY	301	TGCGCGTACAAAGGTAAACTTTTATATTTTATACATTACCTTCAGCCAGCATTTGA	360
Db	1570	TGCGCGTACAAAGGTAAACTTTTATATTTTATACATTACCTTCAGCCAGCATTTGA	1629
QY	361	TATATAATAAAACATTTTCACACATACATTAAGTTAACTATTTTATTTTCTAATGTGCC	420
Db	1630	TATATAATAAAACATTTTCACACATACATTAAGTTAACTATTTTATTTTCTAATGTGCC	1689
QY	421	AGTCTCTTCCTGCTTATGAAAAGCTT	448
Db	1690	AGTCTCTTCCTGCTTATGAAAAGCTT	1717

RESULT 4	HSU51241	1717 bp	DNA linear	PRI 09-OCT-1996
LOCUS	HSU51241			
DEFINITION	Human eosinophil ectaxin receptor (CMKR3)			
ACCESSION	U51241			
VERSION	U51241.1			
KEYWORDS	GI:1480480			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens.			

REFERENCE
AUTHORS

1 (bases 1 to 1717)
Daugherty, B. L., Sticiliano, S. J., Dekartino, J. A., Malkowitz, L.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE Cloning, expression, and characterization of the human eosinophil eotaxin receptor
JOURNAL J. Exp. Med. 183 (5), 2349-2354 (1996)
MEDLINE 96235044

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1717)
Daugherty, B. L.
Direct Submission
Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Laboratories, R80W-107, P.O. Box 2000, Rahway, NJ
07065, USA

FEATURES	Location/Qualifiers
source	1. .1717

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/db_xref="caxon:9606"
205. .1272
/gene="CMKAR3"
205. .1272
CDS

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/note="CC chemokine receptor-3; CCR3"
/codon_start=1
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AVLAALPEFIETEEELFEETLSALVPEPDVYLSWRHPLRLMFIPLVMAIC
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Query Match	100.0%	Score 448;	DB 9;	Length 1717;
Best Local Similarly	100.0%;	Pred. NO. 3.3e-88;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	TAGGTCAGATG	CAGAAAAATTG	CCCTAAAG	GAGGAAGCA	CCAAAGCAGATG	CAACACATT	60
Db	1270	TAGGTCAGATG <th>CAGAAAAATTG</th> <th>CCCTAAAG</th> <th>GAGGAAGCA</th> <th>CCAAAGCAGATG</th> <th>CAACACATT</th> <th>1329</th>	CAGAAAAATTG	CCCTAAAG	GAGGAAGCA	CCAAAGCAGATG	CAACACATT	1329

QY	61	AAATTTCCACACACCTCCTTAAAAACAGCTCCTGAAATTCGACAGCAACACTGAAGTC	120
Db	1330	AAGCCTTCCACACTCACCCTTAAACCACTCCTTCAAACTTCAGAGCAACACTGAAGTC	1389
QY	121	TTGAAGACACTGAAATATATACACACAGCAGTAGTAGATCATGTACCCCTAAGGTCATT	180
Db	1390	TTGAAGACACTGAAATATATACACACAGCAGTAGTAGATCATGTACCCCTAAGGTCATT	1449
QY	181	ACCACAGGCCACAGGGGCTGGGACGCTACTCATCAACCTTAAAAAGCAGAGCTTTGGCT	240
Db	1450	ACCACAGGCCACAGGGGCTGGGACGCTACTCATCAACCTTAAAAAGCAGAGCTTTGGCT	1509
QY	241	TCTCTCTTAAATAGATTACCTACATTTTAATGCACTGAAATGTTAGTAGTACTATA	300
Db	1510	TCTCTCTTAAATAGATTACCTACATTTTAATGCACTGAAATGTTAGTAGTACTATA	1569
QY	301	TGCGCGTCAAAAAGGTAACCTTTTATATTTTATACATTAACTTCAGCCAGCTATTGA	360
Db	1570	TGCGCGTCAAAAAGGTAACCTTTTATATTTTATATACATTAACTTCAGCCAGCTATTGA	1629
QY	361	TATAAATAAAAACATTTTACACACATACAAATAGTTAACTATTTTTCTAAATGTGCTT	420
Db	1630	TATAAATAAAAACATTTTACACACATACAAATAGTTAACTATTTTTCTAAATGTGCTT	1689
QY	421	AGTCTCTCCCTGCCTTAATGAAAAGCTT 448	
Db	1690	AGTCTCTCCCTGCCTTAATGAAAAGCTT 1717	

RESULT 5				
BD006761	BD006761	1915 bp	DNA	linear PAT 31-JAN-2002
LOCUS	Chemokine receptors 88-2B [CD8-3]			and 88C and antibodies thereof.
DEFINITION	BD006761			
ACCESSION	BD006761.1	GI:18635132		
VERSION	JP 2001029089-A/2.			
KEYWORDS				
SOURCE	unidentified.			
ORGANISM	unidentified			

REFERENCE
AUTHORS
TITLE
JOURNAL
I (bases 1 to 1915)
Gary, P.W., Sheiart, V. L., and Rayport, C. J.
Chemokine receptors 88-2B (CCR-3) and 88C and antibodies thereof
Patent: JP 2001029089-A 2 06-FEB-2001;
T005.C00D

COMMENT	OS	Unidentified
	PN	JP 2001029089-A/2

PF	16-MAY-2000 JP	2000143832	
PR	20-DEC-1995 US	08/575667	07-JUN-1996 US
PATRICK W GARY, VICKMI L	SHEICART, CARROLL J	RAYPORT	PC
C12N15/09, C07K14.7//15, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC			
C12N5/10,			
PC	C12N5/10, C12N15/02, C12P21/02, C12P21/08, C12Q1/68, G01N33/15, PC		
G01N33/50,			
PC	G01N33/53, G01N33/5666//A61K39/395, A61K45/00,		
A61P7/02, PC	A61P17/06,		
PC	A61P19/02, A61P29/00, A61P31/12, (C12P21/02, C12R1:91), C12N15/00,		
PC	C12N5/00,		
PC	C12N5/00, C12N15/00		
CC	Strandedness: Single;		
CC	Topology: Linear;		
PH	Key	Location/Qualifiers	
FT	CDS	362, .1426,	
	Location/Qualifiers		

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SOURCE          2 1015      /organism="unidentified"
                /db_xref="taxon:32644"
BASE COUNT      488 a      470 c      373 g      584 t
ORIGIN

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Query Match	100.0%	Score 448	DB 6	Length 1915
Best Local Similarly	100.0%	Pred. No. 3.3e-88		
Matches 448	Conservative 0	Mismatches 0	Indels 0	Gaps 0

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
OY	1	TAGGTCACATGCAAGAAATTCGCTTAAGAAGAGACCAAGAGATGTGAAGCAACACATT	60														
Db	1427	TAGGTCACATGCAAGAAATTCGCTTAAGAAGAGACCAAGAGATGTGAAGCAACACATT	1486														
OY	61	AAGCCTTCACACACTACCTCTAAACAACAGTCCCTTCAAACTTCAGAGCAACACTGAACTC	120														
Db	1487	AAGCCTTCACACACTACCTCTAAACAACAGTCCCTTCAAACTTCAGAGCAACACTGAACTC	1546														
OY	121	TTGAAGACACTGAAATATATACACACAGCAGTAGAGAGATAGATGATGATACCTTAAGTCAATT	180														
Db	1547	TTGAAGACACTGAAATATATACACACAGCAGTAGAGAGATAGATGATGATACCTTAAGTCAATT	1606														
OY	181	ACCACAGGCGAGGGGCTGGGAGCGCTACTCATCATCAACCCCTAAAAAACAGAGCTTGCT	240														
Db	1607	ACCACAGGCGAGGGGCTGGGAGCGCTACTCATCATCAACCCCTAAAAAACAGAGCTTGCT	1666														
OY	241	TCTCTCTCTAAATAGTATACCTACATTTTAATGACACCTGAAATGTTAGATAGTTACTATA	300														
Db	1667	TCTCTCTCTCTAAATAGTATACCTACATTTTAATGACACCTGAAATGTTAGATAGTTACTATA	1726														
OY	301	TGCCCTCAAAAAAGCTAAACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	360														
Db	1727	TGCCCTCAAAAAAGCTAAACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	1786														
OY	361	TATAATATAAACATTTCATACACATATACATTAAGTAACTATTTTATTTTATTTTATTTTATTTT	420														
Db	1787	TATAATATAAACATTTCATACACATATACATTAAGTAACTATTTTATTTTATTTTATTTTATTTT	1846														
OY	421	AGTTCTTTCCCTGCTTTAATGAAGACTT	448														
Db	1847	AGTTCTTTCCCTGCTTTAATGAAGACTT	1874														
RESULT 6																	
AF247361																	
LOCUS	AF247361	5791 bp	DNA	linear	PRI 26-JUN-2002												
DEFINITION	Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.																
ACCESSION	AF247361																
VERSION	AF247361.1	GI:19110542															
KEYWORDS																	
SOURCE	human.																
ORGANISM	Homo sapiens																
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																
TITLE	Vilh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and																
JOURNAL	Michael,N.L.																
MEDLINE	Transcription Regulation of Human Chemokine Receptor CCR3: Evidence																
PUBMED	for a Rare TATA-less Promoter Structure Conserved between																
REFERENCE	Drosophila and Humans																

LOCUS	AC104439	197279 bp	DNA	linear	PRI 20-JUN-2002
DEFINITION	Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.				
ACCESSION	AC104439 AC024739				
VERSION	AC1044439.2 GI:21490240				
KEYWORDS	HTG.				
SOURCE	human.				

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 11731: contig of 11731 bp in length
11732 11831: gap of 100 bp
11832 26218: contig of 14387 bp in length
26219 26318: gap of 100 bp
26319 28347: contig of 2029 bp in length
28348 28447: gap of 100 bp
28448 42160: contig of 13713 bp in length
42161 42360: gap of 200 bp
42361 55059: contig of 12699 bp in length
55060 55159: gap of 100 bp
55160 61578: contig of 6419 bp in length
61579 61678: gap of 100 bp
61679 97342: contig of 35664 bp in length
97343 97442: gap of 100 bp
97443 117655: contig of 20213 bp in length
117656 117755: gap of 100 bp
117756 118727: contig of 972 bp in length
118728 118827: gap of 100 bp
118828 121834: contig of 3007 bp in length
121835 121934: gap of 100 bp
121935 127855: contig of 5921 bp in length
127856 127955: gap of 100 bp
127956 129383: contig of 1428 bp in length
129384 129483: gap of 100 bp
129484 131747: contig of 2264 bp in length
131748 131847: gap of 100 bp
131848 132316: contig of 469 bp in length
132317 132416: gap of 100 bp
132417 134455: contig of 2039 bp in length
134456 134555: gap of 100 bp
134556 135527: contig of 972 bp in length
135528 135627: gap of 100 bp
135628 189051: contig of 53424 bp in length
189052 189151: gap of 100 bp
189152 189476: contig of 325 bp in length
189477 189576: gap of 100 bp
189577 191375: contig of 1799 bp in length
191376 191475: gap of 100 bp
191476 201473: contig of 9998 bp in length
201474 201573: gap of 100 bp
201574 202307: contig of 734 bp in length
202308 202407: gap of 100 bp
202408 204878: contig of 2471 bp in length
204879 204978: gap of 100 bp
204979 213531: contig of 8553 bp in length
213532 213631: gap of 100 bp
213632 218109: contig of 4478 bp in length
218110 218209: gap of 100 bp
218210 219800: contig of 1591 bp in length
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219901 220965: contig of 1065 bp in length.

FEATURES
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/clone="RP6-32g23"

BASE COUNT 62577 a 44674 c 45661 g 65453 t 2600 others
ORIGIN

Query Match 100.0%; Score 448; DB 2; Length 220965;
Best Local Similarity 100.0%; Pred. No. 2.2e-88;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAGGTGATGACAGAAATGCTTAAGAGAGAGACAGAGATGAGCAATTT 60
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Db 141329 TAGGTGATGACAGAAATGCTTAAGAGAGAGACAGAGATGAGCAATTT 141388
OY 61 AAGCTTCACACTGACCTCTAAAAAGAGTCTTCAAACTTCACAGTGAAGCTC 120

|||||
Db 141389 AAGCTTCACACTGACCTCTAAAAAGAGTCTTCAAACTTCACAGTGAAGCTC 141448
OY 121 TTGAAGACACTGAAATTTACACACAGCAGTACGCTAGATGCATCTTAAGTCAATT 180
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Db 141449 TTGAAGACACTGAAATTTACACACAGCAGTACGCTAGATGCATCTTAAGTCAATT 141508
OY 181 ACCACAGGCCAGGGGCTGGGAGCGTCACTCATCAACCTTAAGAGAGCTTGCT 240
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Db 141509 ACCACAGGCCAGGGGCTGGGAGCGTCACTCATCAACCTTAAGAGAGCTTGCT 141568
OY 241 TCTCTCTTAATAGATTAACCTTCAATTTAATGACCTGAATGTTAGATTAATTA 300
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Db 141569 TCTCTCTTAATAGATTAACCTTCAATTTAATGACCTGAATGTTAGATTAATTA 141628
OY 301 TGCCGCTACAAAAGGTAACCTTTATATTTATATTAATTAATTAATTAATTAATTA 360
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Db 141629 TGCCGCTACAAAAGGTAACCTTTATATTTATATTAATTAATTAATTAATTAATTA 141688
OY 361 TATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
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Db 141689 TATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 141748
OY 421 AGTTCTTTCCCTGCTTAATGAAGCTT 448
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Db 141749 AGTTCTTTCCCTGCTTAATGAAGCTT 141776

RESULT 9
HSU49727 1689 bp DNA linear PRI 04-OCT-1996
LOCUS
DEFINITION
Human C-C chemokine receptor 3 (CCR-3) gene, complete cds.
ACCESSION
U49727.1 GI:1477560
VERSION
KEYWORDS
U49727.1 GI:1477560

SOURCE
Homo sapiens.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1689)
Ponath, P.D., Qiu, S., Post, T.W., Wang, J., Wu, L., Gerard, N.P.,
Newman, W., Gerard, C. and Mackay, C.R.
Molecular cloning and characterization of a human eotaxin receptor
expressed selectively on eosinophils
J. Exp. Med. 183 (6), 2437-2448 (1996)
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 1689)
Ponath, P.D.
Direct Submission
TITLE
JOURNAL
Submitted (21-FEB-1996) Paul D. Ponath, Molecular Biology,
Leukosite, Inc., 215 First St., Cambridge, MA 02118, USA
FEATURES
source
1. .1689
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/db_xref="taxon:9606"
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/gene="CCR-3"
181. .1248
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and MCP-3"
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VTGILITLRCPSKKRYKARILRLIEAVFETWYVNAVAILLSYOSILFGDCERT
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FEATURES
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/clone="RP6-32g23"

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Oy		361	TATAAATAAACATTTCACACAATACATAAGTTAACTATTTATTTTCTAATGTGGCT	420
Dd	6457	TATAAATAAATATTTTATATATTAATATAAGTAAAGTAAATATTTATTTTAAATGTGTTT		6516
Oy	421	AGTCTCTTCCTCGCTTAATGAAAGCTT	448	
Dd	6517	AGTTTTTTTTTGTTTAAATGAAGAAGTTT	6544	
RESULT 12				
LOCUS	AC095857			
DEFINITION	Rattus norvegicus clone CH230-10B21, *** SEQUENCING IN PROGRESS			
ACCESSION	AC095857			
VERSION	AC095857.6 GI:22474823			
KEYWORDS	HTG; PHAGEI.			
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
	Rattus.			
REFERENCE	1 (bases 1 to 3202)			
AUTHORS	Muzny,D.,Marie, Metzker,M.,Lee, Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amlin,A., Anguiano,D., Anyalibechi,Y., Ayoyagi,A., Ayodeji,M., Bace,E., Baden,H., Baldwin,D., Bandarainaike,D., Barber,M., Barnstead,M., Beahmed,F., Bliswalo,K., Blair,J., Blankenbury,K., Blythe,P., Brown,M., Bryant,N., Buay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,J.T., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Evans,K., Egan,A., Escotto,M., Eugene,C., Evans,C., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Friser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Georgegeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guvarara,M., Gunaratne,P., Haaland,W., Hamli,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Huilyk,S., Humm,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolyet,A., Kapachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowls,C., Kraft,C.L., Lebow,H., Levin,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensheka,L., Louised,H., Lozardo,R.J., Lu,X., Ma,J., Maheshwarit,M., Mahlndartine,M., Mahmoud,M., Mallory,K., Mangum,A., Mangung,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mathliney,S., Mcleod,M., Mccreall,T., Meenen,E., Milosavljevic,A., Miner,G., Munja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Mundasa,M., Murphy,M., Nair,L., Nankevici,C., Neel,D., Netron,N., Nguyen,N., Norris,S., Nwaketemeh,O., Okwonnu,G., Olarinpusongun,A., Pal,S., Parks,K., Pastelnak,S., Paul,H., Perez,A., Perez,L., Plankoch,C., Plopper,F., Polidexter,A., Popovic,K., Regier,M.A., Reigh,R., Relly,B., Relly,M., Ren,Y., Reeves,K., Regier,M.A., Reigh,R., Relly,B., Relly,M., Ren,Y., Rauter,M., Richards,S., Riggs,F., Rives,C., Rodney,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shelly,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Sosaj,D., Steed,A., Sodergren,E., Song,X.-Z., Sorrelle,R., Soosa,J., Steele,M., Strong,R., Sutton,A., Svatek,A., Tabror,P., Taylor,C., Taylor T., Thomas,N., Thomas,S., Tingey,A., Trejos Z., Usmani,K., Valas,R., Vera V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,J., Wu,J., Yakub,S., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,			

TITLE	Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X.,
JOURNAL	Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R.,
REFERENCE	Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.
AUTHORS	Direct Submission
TITLE	Unpublished
JOURNAL	2 (bases 1 to 320202)
REFERENCE	Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
AUTHORS	of Molecular and Human Genetics, Baylor College of Medicine, One
TITLE	Baylor Plaza, Houston, TX 77030, USA
JOURNAL	3 (bases 1 to 320202)
REFERENCE	Rat Genome Sequencing Consortium.
AUTHORS	Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
TITLE	of Molecular and Human Genetics, Baylor College of Medicine, One
JOURNAL	Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Aug 24, 2002 this sequence version replaced gi:22450501.

	Center: Baylor College of Medicine
	Genome Center
	Center code: BCM
	Web site: http://www.hgsc.bcm.tmc.edu/
	Contact: hgsc-help@bcm.tmc.edu

	Project Information
	Center project name: GDOA
	Center clone name: CH230-10B21

	Summary Statistics
	Sequencing vector: Plasmid:
	Chemistry: Dye-terminator Big Dye: 100% of reads
	Assembly program: Phrap, version 0.990329
	Consensus quality: 239947 bases at least Q40
	Consensus quality: 250769 bases at least Q30
	Consensus quality: 259279 bases at least Q20

	* NOTE: Estimated insert size may differ from sequence length
	* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
	* NOTE: This is a "working draft" sequence. It currently
	* consists of 109 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.

	1
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*	1022
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*	1122
*	2717: contig of 1596 bp in length
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*	2817: gap of unknown length
*	2818
*	4081: contig of 1264 bp in length
*	4082
*	4181: gap of unknown length
*	4182
*	5449: contig of 1268 bp in length
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*	5549: gap of unknown length
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*	7262: contig of 1713 bp in length
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*	7362: gap of unknown length
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*	8704: contig of 1342 bp in length
*	8705
*	8804: gap of unknown length
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*	11817: gap of unknown length
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*	13033: gap of unknown length
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*	14530: contig of 1457 bp in length
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*	14630: gap of unknown length
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*	15906: contig of 1276 bp in length
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*	16006: gap of unknown length
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*	17545: contig of 1539 bp in length
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*	17645: gap of unknown length
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*	19259: contig of 1614 bp in length
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*	19359: gap of unknown length
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*	20931: contig of 1572 bp in length
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*	21031: gap of unknown length
*	21032
*	22282: contig of 1251 bp in length

[illegible]

	RESULT	14		
LOCUS	MNU28406	1440 bp	DNA	linear ROD 27-FEB-1996
DEFINITION	Mus musculus macrophage inflammatory protein-1 alpha receptor-like 2 gene, complete cds.			
ACCESSION	U28406			
VERSION	U28406.1			
KEYWORDS	GI:1203800			
SOURCE	'Mus musculus. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1440) Gao,J.L. and Murphy,P.M. Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor <i>J. Biol. Chem.</i> 270 (29), 17494-17501 (1995)			
REFERENCE	PUBMED	7542241		
AUTHORS	Gao,J.-L. Direct Submission	2 (bases 1 to 1440)		
TITLE	Submitted (05-JUN-1995) Ji-Liang Gao, Lab of Host Defenses, NIAID, National Institutes of Health, Building 10, Room 11N113, Bethesda, MD 20892, USA			
JOURNAL	On Feb 27, 1996 this sequence version replaced gi:1199860. location/Oalifiers			
COMMENT	FEATURES	1..1440		
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gene	227..1306			
CDS	/gene="macrophage inflammatory protein-1 alpha receptor-like 2 gene" /note="WIP-1 alpha receptor like-2" /codon_start=1 /protein_id="AAAB9155.1" /db_xref="GI:1203801" /translation="MAENTDEIKTVSEFETPEYEMAPDCKEKRIKELGSWLPLPVLVSLVFIGLGNNMVAVILIRKYRLOJMTNIENLAISDLPLEFTVPMTIHVMKNBHWGEHGYMKLSGGFYALATSELFFILLITDRYLVAHVAFARLVPTVEATTSTIITMGLAGAALPERIFHEHSODSPFGSCSPRPBGEDSMKRFALRNMNTGLALLPLYMCOSICTITTLTLCPRKKRHAKRLLEVVANIEFTTPNPVLLRSASFHFLETSSCSDSHLDLMQYTEVALTYHCNPVTIVAVEGRFKHLRLFHRNVAYVLYGVTFPC			

BASE COUNT	365 a	325 c	295 g	455 t	LPBKKMERFSSVSPSGEDELISVVF*
ORIGIN					
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Best Local Similarity		65.6%;	Pred. No. 0.02;		
Matches 82;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps	
QY	13	AGAAATTTGGCTTAAGAGGAAGGACCAAGAGATGTAAGCAACACTTAAAGCTTCCACA	72		
Db	1315	AGAAATTTGTCACTTATTCCATGATGCAAGAGTGAAGCAACATTTAAGTCAGTCACA	1374		
QY	73	CTCACTCTCTAAACAGTGCCTTCAAACTTCCAGTCAACAACCTGAAGCTCTTGAAGACACTG	132		
		+			
Db	1375	ATGACCTCTGATGCTACGATCATTTGTACTTTCATGCAATGCTGATGCTCTCAAAAGCACTGT	1434		
QY	133	AAATA 137			
Db	1435	AAACA 1439			

RESULT 15	AX344574/c	AX344574	349980 bp	DNA	linear	PAT 01-FEB-2002
LOCUS		AX344574	Sequence 25 from Patent WO0200932.			
DEFINITION		AX344574				
ACCESSION		AX344574				
VERSION		AX344574.1	GI:18492460			
KEYWORDS						
SOURCE			synthetic construct.			
ORGANISM			artificial sequences.			
REFERENCE		1				
AUTHORS		Olek, A., Piepenbrock, C. and Berlin, K.				
TITLE		Diagnosis of known genetic parameters within the mhc				
JOURNAL		Patent: WO 0200932-A 25 03-JUN-2002;				
FEATURES		Epigenomics AG (DE)				
Source		Location/Qualifiers				
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ORIGIN						
Query Match		10.8%:	Score 48.4:	DB 6:	Length 349980:	
Best Local Similarity		45.5%:	Pred. No. 0.7:			
Matches 172:		Conservative 0:	Mismatches 206:	Indels	Gaps	0:
OY 15	AAATTTGCTTAAGAGAGAGCAAGAGATGAAGCAACATTAAGCTTCACACT 74					
Db 296365	AAACTACATTAACACCAAAATACCTAACGAATATTAATAAAAAAATTTAACTTTACACT 296366					
OY 75	CACCTTAAACAGTCCCTTCAACTCCAGTGCACACTGTAAGCTCTTGAAGACACTAA 134					
Db 296305	ATTACTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTCTTCATAA 296306					
OY 135	ATATACACACAGACGTACAGTACATGATGCATTTACCTTAAGTGTCAATTACACAGGCCAGG 194					

Db 296245 ATTTAAACCAAAATACCATTTAAACCAACAATCCCATTAACAATAATACATCAAAAA 296186
OY 195 GCTGGGCGAGGTACATCATCAACCTTAAAAAGCAGAGCTTGTCTCTCTCTAAAAAT 254
Db 296185 AAAATAATCACTCTATTTAAATAATACATACATATATATCTTATTACACACATATCCA 296126
OY 255 GAGTTACCTACATTTTAATGCAACCTGAATGTTAGATAGTTACTATATGCCGTACAAAAA 314
Db 296125 CATTAACAAAAACATTAATAATCAACCCCAATACCCATCATTAATATCTACTTAAAAAAA 296066
OY 315 GGTAAACTTTTATATTTTATACATTAACCTTCAGCCAGCTATTTGATATATAATAAAAACAT 374
Db 296065 TATTAATACATATACACCATTAATAATTTATACACACAAAAAAATAATAATTCATTCCT 296006
OY 375 TTTCACACATACATTA 392
Db 296005 TTACAAAAATATAATTA 295988

Search completed: February 24, 2003, 15:30:17
Job time : 1751.75 secs